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Sequence Listing was accepted.
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Reviewer: Anne Corrigan
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Validated By CRFValidator v 1.0.3

Application No: 09492028 Version No: 2.0

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No. of SeqIDs Defined: 14
Actual SeqID Count: 14

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<110> APPLICANT: Zuker, Charles S.
The Regents of the University of California
<120> TITLE OF INVENTION: Assays for Sensory Modulators Using a Sensory Cell Specific G-Protein Alpha Subunit
<130> FILE REFERENCE: 02307E-092610US

<140> CURRENT APPLICATION NUMBER:09492028
<141> CURRENT FILING DATE:2008-11-20
<150> PRIOR APPLICATION NUMBER: US 60/117,367
<151> PRIOR FILING DATE: 1999-01-27
<160> NUMBER OF SEQ ID NOS: 14
<170> SOFTWARE: PatentIn Ver. 2.1

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<211> LENGTH: 1503
<212> TYPE: DNA
<213> ORGANISM: Mus sp.
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (157)..(1224)
<223> OTHER INFORMATION: mouse taste cell specific G-protein alpha 14 subunit (TC-Galpha14)
<400> SEQUENCE: 1

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ctccaggtcc ctgtcgctcc gtcgaggtgg caagcc atg gcc ggc tgc tgc tgt   174
                                        Met Ala Gly Cys Cys Cys
                                          1               5
ttg tct gcg gag gag aaa gag tct cag cgc atc agc gcg gag atc gag   222
Leu Ser Ala Glu Glu Lys Glu Ser Gln Arg Ile Ser Ala Glu Ile Glu
             10                  15                  20
cgg cac gtt cgc cgc gac aag aag gac gcg cgc cgg gag ctc aag ctg   270
Arg His Val Arg Arg Asp Lys Lys Asp Ala Arg Arg Glu Leu Lys Leu
         25                  30                  35
ctg ttg ctg gga acc ggt gag agt ggg aaa agc acc ttt atc aag cag   318
Leu Leu Leu Gly Thr Gly Glu Ser Gly Lys Ser Thr Phe Ile Lys Gln
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atg agg ata atc cat ggg tct ggc tac agt gat gaa gat aga aag ggc   366
Met Arg Ile Ile His Gly Ser Gly Tyr Ser Asp Glu Asp Arg Lys Gly
 55                  60                  65                  70
ttc acg aag ctg gtt tac caa aac ata ttc acg gcc atg caa gcc atg   414
Phe Thr Lys Leu Val Tyr Gln Asn Ile Phe Thr Ala Met Gln Ala Met
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atc aga gca atg gat acc ctg agg ata caa tac atg tgt gag cag aat   462
Ile Arg Ala Met Asp Thr Leu Arg Ile Gln Tyr Met Cys Glu Gln Asn
             90                  95                 100
aag gaa aat gcc cag atc atc agg gaa gtg gaa gta gac aag gtc act   510
Lys Glu Asn Ala Gln Ile Ile Arg Glu Val Glu Val Asp Lys Val Thr
        105                 110                 115
gca ctc tct aga gac cag gtg gca gcc atc aag cag ctg tgg ctg gat   558
Ala Leu Ser Arg Asp Gln Val Ala Ala Ile Lys Gln Leu Trp Leu Asp
    120                 125                 130
ccc gga atc cag gag tgt tac gac agg agg agg gag tac cag ctg tca   606
Pro Gly Ile Gln Glu Cys Tyr Asp Arg Arg Arg Glu Tyr Gln Leu Ser
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gac tct gcc aaa tat tac ctg acg gac att gag cgt atc gcc atg ccc   654
Asp Ser Ala Lys Tyr Tyr Leu Thr Asp Ile Glu Arg Ile Ala Met Pro
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tct ttc gtg cca aca caa cag gat gtg ctt cgt gtt aga gtg ccc acc   702
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            170                 175                 180
act ggc atc ata gaa tat cca ttc gac ctg gaa aac atc atc ttc cga   750
Thr Gly Ile Ile Glu Tyr Pro Phe Asp Leu Glu Asn Ile Ile Phe Arg
        185                 190                 195
atg gtg gat gtt ggt ggc cag cga tct gaa cga cgg aaa tgg att cac   798
Met Val Asp Val Gly Gly Gln Arg Ser Glu Arg Arg Lys Trp Ile His
    200                 205                 210
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Cys Phe Glu Ser Val Thr Ser Ile Ile Phe Leu Val Ala Leu Ser Glu
215                 220                 225                 230
tat gac cag gtt ctg gct gag tgt gac aat gag aac cgc atg gag gag   894
Tyr Asp Gln Val Leu Ala Glu Cys Asp Asn Glu Asn Arg Met Glu Glu
                235                 240                 245
agc aaa gcc ctg ttt aga acc atc atc acc tac ccc tgg ttt ctg aac   942
Ser Lys Ala Leu Phe Arg Thr Ile Ile Thr Tyr Pro Trp Phe Leu Asn
            250                 255                 260
tcc tcc gtg att ctg ttc tta aac aag aag gat ctt cta gag gag aaa   990
Ser Ser Val Ile Leu Phe Leu Asn Lys Lys Asp Leu Leu Glu Glu Lys
        265                 270                 275
atc atg tac tct cat cta att agc tac ttc cca gag tac aca gga cca   1038
Ile Met Tyr Ser His Leu Ile Ser Tyr Phe Pro Glu Tyr Thr Gly Pro
    280                 285                 290
aag caa gat gtc aaa gcg gcc agg gac ttt atc ctg aag ctg tat caa   1086
Lys Gln Asp Val Lys Ala Ala Arg Asp Phe Ile Leu Lys Leu Tyr Gln
295                 300                 305                 310
gac cag aat cct gac aaa gag aag gtt atc tat tct cac ttc act tgt   1134
Asp Gln Asn Pro Asp Lys Glu Lys Val Ile Tyr Ser His Phe Thr Cys
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gct aca gac acc gag aat atc cgc ttt gtg ttt gct gct gtc aaa gac   1182
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aca atc cta cag cta aac cta cgg gag ttc aac ttg gtg taa           1224
Thr Ile Leu Gln Leu Asn Leu Arg Glu Phe Asn Leu Val
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<210> SEQ ID NO 2
<211> LENGTH: 355
<212> TYPE: PRT
<213> ORGANISM: Mus sp.
<220> FEATURE:
<223> OTHER INFORMATION: mouse taste cell specific G-protein alpha 14 subunit (TC-Galpha14)

<400> SEQUENCE: 2

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Thr Ala Met Gln Ala Met Ile Arg Ala Met Asp Thr Leu Arg Ile Gln
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Tyr Met Cys Glu Gln Asn Lys Glu Asn Ala Gln Ile Ile Arg Glu Val
            100                 105                 110
Glu Val Asp Lys Val Thr Ala Leu Ser Arg Asp Gln Val Ala Ala Ile
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Lys Gln Leu Trp Leu Asp Pro Gly Ile Gln Glu Cys Tyr Asp Arg Arg
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Arg Glu Tyr Gln Leu Ser Asp Ser Ala Lys Tyr Tyr Leu Thr Asp Ile
145                 150                 155                 160
Glu Arg Ile Ala Met Pro Ser Phe Val Pro Thr Gln Gln Asp Val Leu
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Arg Val Arg Val Pro Thr Thr Gly Ile Ile Glu Tyr Pro Phe Asp Leu
            180                 185                 190
Glu Asn Ile Ile Phe Arg Met Val Asp Val Gly Gly Gln Arg Ser Glu
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Arg Arg Lys Trp Ile His Cys Phe Glu Ser Val Thr Ser Ile Ile Phe
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Leu Val Ala Leu Ser Glu Tyr Asp Gln Val Leu Ala Glu Cys Asp Asn
225                 230                 235                 240
Glu Asn Arg Met Glu Glu Ser Lys Ala Leu Phe Arg Thr Ile Ile Thr
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Tyr Pro Trp Phe Leu Asn Ser Ser Val Ile Leu Phe Leu Asn Lys Lys
            260                 265                 270
Asp Leu Leu Glu Glu Lys Ile Met Tyr Ser His Leu Ile Ser Tyr Phe
        275                 280                 285
Pro Glu Tyr Thr Gly Pro Lys Gln Asp Val Lys Ala Ala Arg Asp Phe
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Ile Leu Lys Leu Tyr Gln Asp Gln Asn Pro Asp Lys Glu Lys Val Ile
305                 310                 315                 320
Tyr Ser His Phe Thr Cys Ala Thr Asp Thr Glu Asn Ile Arg Phe Val
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Asn Leu Val
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<212> TYPE: DNA
<213> ORGANISM: Rattus sp.
<220> FEATURE:
<223> OTHER INFORMATION: rat G-protein coupled receptor B3 (GPCR-B3)
<400> SEQUENCE: 3

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<212> TYPE: DNA
<213> ORGANISM: Mus sp.
<220> FEATURE:
<223> OTHER INFORMATION: mouse G-protein coupled receptor B3 (GPCR-B3)
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<210> SEQ ID NO 5
<211> LENGTH: 2333
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<223> OTHER INFORMATION: human G-protein coupled receptor (GPCR-B3)
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